

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,241

DATE: 12/11/2001

TIME: 11:31:21

Input Set : N:\jumbos\008000051CNUS01.txt

Output Set: N:\CRF3\12112001\I993241.raw

4 <110> APPLICANT: KAKKIS, EMIL D.
6 <120> TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
7 RECOMBINANT ALPHA-L-IDURONDINASE
9 <130> FILE REFERENCE: 008000051CNUS01
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/993,241
12 <141> CURRENT FILING DATE: 2001-11-13
14 <150> PRIOR APPLICATION NUMBER: 09/711,205
15 <151> PRIOR FILING DATE: 2000-11-09
17 <150> PRIOR APPLICATION NUMBER: 09/439,923
18 <151> PRIOR FILING DATE: 1999-11-12
20 <160> NUMBER OF SEQ ID NOS: 2
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 6200
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1558)...(3510)
33 <400> SEQUENCE: 1

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36	cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
37	ttagggttag	gcgttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
38	gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
39	tggagtcccg	cgttacataa	cttacggtaa	atggcccgc	tggctgaccg	cccaacgacc	360
40	cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgcccaata	gggactttcc	420
41	attgacgtca	atgggtggac	tatttacggg	aaactgccca	cttggcagta	catcaagtgt	480
42	atcatatgcc	aagtagcccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
43	atgccagta	catgacctta	tgggaacttc	ctacttgcca	gtacatctac	gtattagtca	600
44	tcgctattac	catggtgatg	cggttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
45	actcacggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttg	ttttggcacc	720
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47	gtaggcgtgt	acgggtgggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840
48	ctgcttaact	ggcttatoga	aattaatacg	actcactata	gggagaccca	agcttcgcag	900
49	aattcctgcg	gctgctacag	tgtgtccagc	gtcctgcctg	gctgtgctga	gcgctggaac	960
50	agtggcgc	cattcaagtg	cacagttacc	catcctgagt	ctggcacctt	aactggcaca	1020
51	attgccaaag	tcacaggtga	gctcagatgc	ataccaggac	attgtatgac	gttccctgct	1080
52	cacatgcctg	ctttcttctt	ataatacaga	tgctcaacta	actgctcatg	tccttatata	1140
53	acagagggaa	attggagcta	tctgaggaa	tgcccagaag	ggaagggcag	aggggtcttg	1200
54	ctctccttgt	ctgagccata	actcttcttt	ctacctcca	gtgaacacct	tcccacccca	1260
55	ggtccacctg	ctaccgccgc	cgtcggagga	gctggccctg	aatgagctct	tgtccctgac	1320
56	atgcctggtg	cgagctttca	accctaaaga	agtgcgtgtg	cgatggctgc	atggaaatga	1380
57	ggagctgtcc	ccagaaagct	acctagtgtt	tgagccccta	aaggagccag	gcgagggagc	1440
58	caccacctac	ctggtgacaa	gcgtgttgcg	tgtatcagct	gaaagcttga	tatogaattc	1500
59	cggaggcgga	accggcagtg	cagcccgaag	ccccgcagtc	cccgagcacg	cgtggccc atg	1560
60						Met	

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61																	1
63	cgt	ccc	ctg	cgc	ccc	cgc	gcc	gcg	ctg	ctg	gcg	ctc	ctg	gcc	tcg	ctc	1608
64	Arg	Pro	Leu	Arg	Pro	Arg	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Ala	Ser	Leu	
65	5				10				15								
67	ctg	gcc	gcg	ccc	ccg	gtg	gcc	ccg	gcc	gag	gcc	ccg	cac	ctg	gtg	cat	1656
68	Leu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Glu	Ala	Pro	His	Leu	Val	His	
69	20				25				30								
71	gtg	gac	gcg	gcc	cgc	gcg	ctg	tgg	ccc	ctg	cgg	cgc	ttc	tgg	agg	agc	1704
72	Val	Asp	Ala	Ala	Arg	Ala	Leu	Trp	Pro	Leu	Arg	Arg	Phe	Trp	Arg	Ser	
73	35				40				45								
75	aca	ggc	ttc	tgc	ccc	ccg	ctg	cca	cac	agc	cag	gct	gac	cag	tac	gtg	1752
76	Thr	Gly	Phe	Cys	Pro	Pro	Leu	Pro	His	Ser	Gln	Ala	Asp	Gln	Tyr	Val	
77	50				55				60				65				
79	ctc	agc	tgg	gac	cag	cag	ctc	aac	ctc	gcc	tat	gtg	ggc	gcc	gtc	cct	1800
80	Leu	Ser	Trp	Asp	Gln	Gln	Leu	Asn	Leu	Ala	Tyr	Val	Gly	Ala	Val	Pro	
81	70				75				80								
83	cac	cgc	ggc	atc	aag	cag	gtc	cgg	acc	cac	tgg	ctg	ctg	gag	ctt	gtc	1848
84	His	Arg	Gly	Ile	Lys	Gln	Val	Arg	Thr	His	Trp	Leu	Leu	Glu	Leu	Val	
85	85				90				95								
87	acc	acc	agg	ggg	tcc	act	gga	cgg	ggc	ctg	agc	tac	aac	ttc	acc	cac	1896
88	Thr	Thr	Arg	Gly	Ser	Thr	Gly	Arg	Gly	Leu	Ser	Tyr	Asn	Phe	Thr	His	
89	100				105				110								
91	ctg	gac	ggg	tac	ctg	gac	ctt	ctc	agg	gag	aac	cag	ctc	ggg	ttt	gag	1944
92	Leu	Asp	Gly	Tyr	Leu	Asp	Leu	Leu	Arg	Glu	Asn	Gln	Leu	Gly	Phe	Glu	
93	115				120				125								
95	ctg	atg	ggc	agc	gcc	tcg	ggc	cac	ttc	act	gac	ttt	gag	gac	aag	cag	1992
96	Leu	Met	Gly	Ser	Ala	Ser	Gly	His	Phe	Thr	Asp	Phe	Glu	Asp	Lys	Gln	
97	130				135				140				145				
99	cag	gtg	ttt	gag	tgg	aag	gac	ttg	gtc	tcc	agc	ctg	gcc	agg	aga	tac	2040
100	Gln	Val	Phe	Glu	Trp	Lys	Asp	Leu	Val	Ser	Ser	Leu	Ala	Arg	Arg	Tyr	
101	150				155				160								
103	atc	ggt	agg	tac	gga	ctg	gcg	cat	gtt	tcc	aag	tgg	aac	ttc	gag	acg	2088
104	Ile	Gly	Arg	Tyr	Gly	Leu	Ala	His	Val	Ser	Lys	Trp	Asn	Phe	Glu	Thr	
105	165				170				175								
107	tgg	aat	gag	cca	gac	cac	cac	gac	ttt	gac	aac	gtc	tcc	atg	acc	atg	2136
108	Trp	Asn	Glu	Pro	Asp	His	His	Asp	Phe	Asp	Asn	Val	Ser	Met	Thr	Met	
109	180				185				190								
111	caa	ggc	ttc	ctg	aac	tac	tac	gat	gcc	tgc	tcg	gag	ggt	ctg	cgc	gcc	2184
112	Gln	Gly	Phe	Leu	Asn	Tyr	Tyr	Asp	Ala	Cys	Ser	Glu	Gly	Leu	Arg	Ala	
113	195				200				205								
115	gcc	agc	ccc	gcc	ctg	cgg	ctg	gga	ggc	ccc	ggc	gac	tcc	ttc	cac	acc	2232
116	Ala	Ser	Pro	Ala	Leu	Arg	Leu	Gly	Gly	Pro	Gly	Asp	Ser				

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127	tcc ctc cac agg aag ggt gcg cgc agc tcc atc tcc atc ctg gag cag	2376
128	Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln	
129	260 265 270	
131	gag aag gtc gtc gcg cag cag atc cgg cag ctc ttc ccc aag ttc gcg	2424
132	Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala	
133	275 280 285	
135	gac acc ccc att tac aac gac gag gcg gac ccg ctg gtg ggc tgg tcc	2472
136	Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp Ser	
137	290 295 300 305	
139	ctg cca cag ccg tgg agg gcg gac gtg acc tac gcg gcc atg gtg gtg	2520
140	Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val Val	
141	310 315 320	
143	aag gtc atc gcg cag cat cag aac ctg cta ctg gcc aac acc acc tcc	2568
144	Lys Val Ile Ala Gln His Gln Asn Leu Leu Ala Asn Thr Thr Ser	
145	325 330 335	
147	gcc ttc ccc tac gcg ctc ctg agc aac gac aat gcc ttc ctg agc tac	2616
148	Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr	
149	340 345 350	
151	cac ccg cac ccc ttc gcg cag cgc acg ctc acc gcg cgc ttc cag gtc	2664
152	His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val	
153	355 360 365	
155	aac aac acc cgc ccg ccg cac gtg cag ctg ttg cgc aag ccg gtg ctc	2712
156	Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu	
157	370 375 380 385	
159	acg gcc atg ggg ctg ctg gcg ctg ctg gat gag gag cag ctc tgg gcc	2760
160	Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu Trp Ala	
161	390 395 400	
163	gaa gtg tcg cag gcc ggg acc gtc ctg gac agc aac cac acg gtg ggc	2808
164	Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val Gly	
165	405 410 415	
167	gtc ctg gcc agc gcc cac cgc ccc cag ggc ccg gcc gac gcc tgg cgc	2856
168	Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala Trp Arg	
169	420 425 430	
171	gcc gcg gtg ctg atc tac gcg agc gac gac acc cgc gcc cac ccc aac	2904
172	Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn	
173	435 440 445	
175	cgc agc gtc gcg gtg acc ctg cgg ctg cgc ggg gtg ccc ccc ggc ccg	2952
176	Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro	
177	450 455 460 465	
179	ggc ctg gtc tac gtc acg cgc tac ctg gac aac ggg ctc tgc agc ccc	3000
180	Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro	
181	470 475 480	
183	gac ggc gag tgg cgg cgc ctg ggc cgg ccc gtc ttc ccc acg gca gag	3048
184	Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu	
185	485 490 495	
187	cag ttc cgg cgc tag cgc gcg gct gag gac ccg gtg gcc gcg gcg ccc	3096
188	Gln Phe Arg Arg * Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro	
189	500 505 510	
191	cgc ccc tta ccc gcc ggc ggc cgc ctg agg ctg cgc ccc gcg ctg cgg	3144

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193	515 520 525	
195	ctg ccg tcg ctt ttg ctg gtg cac gtg tgt gcg cgc ccc gag aag ccg	3192
196	Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro	
197	530 535 540	
199	ccc ggg cag gtc acg cgg ctc cgc gcc ctg ccc ctg acc caa ggg cag	3240
200	Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln	
201	545 550 555 560	
203	ctg gtt ctg gtc tgg tcg gat gaa cac gtg ggc tcc aag tgc ctg tgg	3288
204	Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp	
205	565 570 575	
207	aca tac gag atc cag ttc tct cag gac ggt aag gcg tac acc ccg gtc	3336
208	Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val	
209	580 585 590	
211	agc agg aag cca tcg acc ttc aac ctc ttt gtg ttc agc cca gac aca	3384
212	Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr	
213	595 600 605	
215	ggt gct gtc tct ggc tcc tac cga gtt cga gcc ctg gac tac tgg gcc	3432
216	Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr Trp Ala	
217	610 615 620	
219	cga cca ggc ccc ttc tcg gac cct gtg ccg tac ctg gag gtc cct gtg	3480
220	Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val	
221	625 630 635 640	
223	cca aga ggg ccc cca tcc ccg ggc aat cca tgagcctgtg ctgagcccca	3530
224	Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro	
225	645 650	
227	gtgggttgca cctccaccgg cagtcagcga gctggggctg cactgtgccc atgctgccct	3590
228	cccatacccc cctttgcaat atatttttat atttttaaaaa aaaaaaaaaa aaaaaaaaaa	3650
229	aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aattcctgca	3710
230	gcccggggga tccactagtt ctagagggcc cgttttaacc cgctgatcag cctcgactgt	3770
231	gccttctagt tgccagccat ctgttgtttg cccctccccc gtgccttcc tgcacctgga	3830
232	aggtgccact cccactgtcc tttcctaata aaatgaggaa attgcategc attgtctgag	3890
233	taggtgtcat tctattctgg ggggtggggg ggggcaggac agcaaggggg aggattggga	3950
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237	gcctaattgag tgagctaaact cacattaatt gcgttgcgct cactgcccgc tttccagtcg	4190
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243	tcaagtcaga ggtggcgaaa ccgacagga ctataaagat accaggcggt tccccctgga	4550
244	agctccctcg tgcgctctcc tgttccgacc ctgccgctta ccggatacct gtccgccttt	4610
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246	taggtcgttc gctccaagct gggtgtgtg cacgaacccc ccgttcagcc cgaccgctgc	4730
247	gccttatccg gtaactatcg tcttgagtc aacccggtaa gacacgactt atcgccactg	4790
248	gcagcagcca ctggtaacag gattagcaga gcgaggtatg taggcgggtg tacagagttc	4850
249	ttgaagtggg ggcctaacta cggctacact agaaggacag tatttggtat ctgcgctctg	4910

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251 gctggttagcg gtggtttttt tgtttgcaag cagcagatta cgcgcagaaa aaaaggatct 5030
252 caagaagatc ctttgatctt ttctacggg tctgacgctc agtggaacga aaactcacgt 5090
253 taagggattt tggatcatgag attatcaaaa aggatcttca cctagatcct tttaaattaa 5150
254 aatgaagtt ttaaataaat cttaaagtata tatgagtaaa cttggtctga cagttacca 5210
255 tgcttaatca gtgaggcacc tatctcagcg atctgtctat ttcgttcacc catagttgcc 5270
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257 gcaatgatac cgcgagaccc acgtcacccg gctccagatt tatcagcaat aaaccagcca 5390
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260 gccattgcta caggcatcgt ggtgtcacgc tcgtcgtttg gtatggcttc attcagctcc 5570
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283 His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
284 35 40 45
285 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
286 50 55 60
287 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
288 65 70 75 80
289 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
290 85 90 95
291 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
292 100 105 110
293 His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Gly Phe
294 115 120 125
295 Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys
296 130 135 140
297 Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg
298 145 150 155 160
299 Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu
300 165 170 175

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number